



SEQUENCE LISTING

03 <110> CIEPLAK, WITOLD

<120> PERTUSSIN TOXIN GENE: CLONING AND EXPRESSION OF
PROTECTIVE ANTIGEN

<130> 2026-4253US7c

<140> 09/770,875

<141> 2001-01-26

<150> 07/311,612

<151> 1989-02-15

<150> 07/542,149

<151> 1990-06-22

<150> 08/483,326

<151> 1995-06-07

<150> 09/128,911

<151> 1998-08-04

<160> 28

<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

<213> Bordetella pertussis

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<212> PRT

<213> Bordetella pertussis

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Leu Leu Ala Ser Gly Ala Met Thr His Leu Ser Pro Ala Leu Ala Asp
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Val Pro Tyr Val Leu Val Lys Thr Asn Met Val Val Thr Ser Val Ala
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Met Lys Pro Tyr Glu Val Thr Pro Thr Arg Met Leu Val
 50 55 60

<210> 3

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<212> DNA

<213> Bordetella pertussis

<220>

<223> Purine (P) R=G or A; Y=T or C; N=A, C, G, or T

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<221> modified_base

<222> (6)

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<222> (15)

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17

<210> 4

<211> 30

<212> PRT

<213> Bordetella pertussis

<220>

<223> Xaa = Any amino acid; the 8th Val and 4th Pro are questionable.

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<221> VARIANT

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Ala Met Lys Pro Tyr Glu Val Val Pro Pro Arg Met Leu Val
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<212> DNA

<213> Bordetella pertussis

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tttgccgccc aaggcgccac gccggtcac gccacgccgg atcagaccgcgggtttcatc 180

gcagacgaga tccagcgctg ggccggcgctc gtgcgcgaaa ccggcgccaa gctgaagtag 240

cagcgcagcc ctccaacgcg ccatccccgt ccggccggca ccatcccgca tacgtgttg 300

caaccgccaa cgcgcatgcg tgcagattcg tcgtacaaaa ccctcgattc ttccgtacat 360
 cccgctactg caatccaaca cggcatgaac gctccttcgg cgcaaagtcg cgcgatggta 420
 ccggtcaccg tccggaccgt gctgaccccc ctgccatggg gtgatcccta aaataggcac 480
 catcaaaacg cagaggggaa gacgggatgc gttgcactcg ggcaattcgc caaaccgcaa 540
 gaacaggctg gctgacgtgg ctggcgattc ttgccgtcac ggcgcccgtg acttcgccgg 600
 catggggcc gac gat cct ccc gcc acc gta tac cgc tat gac tcc cgc ccg 650
 Asp Asp Pro Pro Ala Thr Val Tyr Arg Tyr Asp Ser Arg Pro
 1 5 10
 ccg gag gac gtt ttc cag aac gga ttc acg gcg tgg gga aac aac gac 698
 Pro Glu Asp Val Phe Gln Asn Gly Phe Thr Ala Trp Gly Asn Asn Asp
 15 20 25 30
 aat gtg ctc gac cat ctg acc gga cgt tcc tgc cag gtc ggc agc agc 746
 Asn Val Leu Asp His Leu Thr Gly Arg Ser Cys Gln Val Gly Ser Ser
 35 40 45
 aac agc gct ttc gtc tcc acc agc agc agc cgg cgc tat acc gag gtc 794
 Asn Ser Ala Phe Val Ser Thr Ser Ser Ser Arg Arg Tyr Thr Glu Val
 50 55 60
 tat ctc gaa cat cgc atg cag gaa gcg gtc gag gcc gaa cgc gcc ggc 842
 Tyr Leu Glu His Arg Met Gln Glu Ala Val Glu Ala Glu Arg Ala Gly
 65 70 75
 agg ggc acc ggc cac ttc atc ggc tac atc tac gaa gtc cgc gcc gac 890
 Arg Gly Thr Gly His Phe Ile Gly Tyr Ile Tyr Glu Val Arg Ala Asp
 80 85 90
 aac aat ttc tac ggc gcc gcc agc tcg tac ttc gaa tac gtc gac act 938
 Asn Asn Phe Tyr Gly Ala Ala Ser Ser Tyr Phe Glu Tyr Val Asp Thr
 95 100 105 110
 tat ggc gac aat gcc ggc cgt atc ctc gcc ggc gcg ctg gcc acc tac 986
 Tyr Gly Asp Asn Ala Gly Arg Ile Leu Ala Gly Ala Leu Ala Thr Tyr
 115 120 125
 cag agc gaa tat ctg gca cac cgg cgc att ccg ccc gaa aac atc cgc 1034
 Gln Ser Glu Tyr Leu Ala His Arg Arg Ile Pro Pro Glu Asn Ile Arg
 130 135 140
 agg gta acg cgg gtc tat cac aac ggc atc acc ggc gag acc acg acc 1082
 Arg Val Thr Arg Val Tyr His Asn Gly Ile Thr Gly Glu Thr Thr Thr

145	150	155	
acg gag tat tcc aac gct cgc tac gtc agc cag cat act cgc gcc aat			1130
Thr Glu Tyr Ser Asn Ala Arg Tyr Val Ser Gln His Thr Arg Ala Asn			
160	165	170	
ccc aac ccc tac aca tcg cga agg tcc gta gcg tcg atc gtc ggc aca			1178
Pro Asn Pro Tyr Thr Ser Arg Arg Ser Val Ala Ser Ile Val Gly Thr			
175	180	185	190
ttg gtg cgc atg gcg ccg gtg ata ggc gct tgc atg gcg cgg cag gcc			1226
Leu Val Arg Met Ala Pro Val Ile Gly Ala Cys Met Ala Arg Gln Ala			
195	200	205	
gaa agc tcc gag gcc atg gca gcc tgg tcc gaa cgc gcc ggc gag gcg			1274
Glu Ser Ser Glu Ala Met Ala Ala Trp Ser Glu Arg Ala Gly Glu Ala			
210	215	220	
atg gtt ctc gtg tac tac gaa agc atc gcg tat tcg ttctagacct			1320
Met Val Leu Val Tyr Tyr Glu Ser Ile Ala Tyr Ser			
225	230		
ggcccagccc cgcccaactc cggttaattca acagcatgcc gatcgaccgc aagacgtctt			1380
gccatctcct gtccgttctg ccgttggtccc tcctcggatc tcacgtggcg cgg gcc			1436
		Ala	
		235	
tcc acg cca ggc atc gtc att ccg ccg cag gaa cag att acc cag cat			1484
Ser Thr Pro Gly Ile Val Ile Pro Pro Gln Glu Gln Ile Thr Gln His			
240	245	250	
ggc agc ccc tat gga cgc tgc gcg aac aag acc cgt gcc ctg acc gtg			1532
Gly Ser Pro Tyr Gly Arg Cys Ala Asn Lys Thr Arg Ala Leu Thr Val			
255	260	265	
gcg gaa ttg cgc ggc agc ggc gat ctg cag gag tac ctg cgt cat gtg			1580
Ala Glu Leu Arg Gly Ser Gly Asp Leu Gln Glu Tyr Leu Arg His Val			
270	275	280	
acg cgc ggc tgg tca ata ttt gcg ctc tac gat ggc acc tat ctc ggc			1628
Thr Arg Gly Trp Ser Ile Phe Ala Leu Tyr Asp Gly Thr Tyr Leu Gly			
285	290	295	
ggc gaa tat ggc ggc gtg atc aag gac gga aca ccc ggc ggc gca ttc			1676
Gly Glu Tyr Gly Gly Val Ile Lys Asp Gly Thr Pro Gly Gly Ala Phe			
300	305	310	315

gac ctg aaa acg acg ttc tgc atc atg acc acg cgc aat acg ggt caa 1724
 Asp Leu Lys Thr Thr Phe Cys Ile Met Thr Thr Arg Asn Thr Gly Gln
 320 325 330

ccc gca acg gat cac tac tac agc aac gtc acc gcc act cgc ctg ctc 1772
 Pro Ala Thr Asp His Tyr Tyr Ser Asn Val Thr Ala Thr Arg Leu Leu
 335 340 345

tcc agc acc aac agc agg cta tgc gcg gtc ttc gtc aga agc ggg caa 1820
 Ser Ser Thr Asn Ser Arg Leu Cys Ala Val Phe Val Arg Ser Gly Gln
 350 355 360

ccg gtc att ggc gcc tgc acc agc ccg tat gac ggc aag tac tgg agc 1868
 Pro Val Ile Gly Ala Cys Thr Ser Pro Tyr Asp Gly Lys Tyr Trp Ser
 365 370 375

atg tac agc cgg ctg cgg aaa atg ctt tac ctg atc tac gtg gcc ggc 1916
 Met Tyr Ser Arg Leu Arg Lys Met Leu Tyr Leu Ile Tyr Val Ala Gly
 380 385 390 395

atc tcc gta cgc gtc cat gtc agc aag gaa gaa cag tat tac gac tat 1964
 Ile Ser Val Arg Val His Val Ser Lys Glu Glu Gln Tyr Tyr Asp Tyr
 400 405 410

gag gac gca acg ttc gag act tac gcc ctt acc ggc atc tcc atc tgc 2012
 Glu Asp Ala Thr Phe Glu Thr Tyr Ala Leu Thr Gly Ile Ser Ile Cys
 415 420 425

aat cct gga tca tcc tta tgctgagacg cttccccact cgaaccaccg 2060
 Asn Pro Gly Ser Ser Leu
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ccggcgcgat gacgcatttt tccccgcgcc tg gcc gac gtt cct tat gtg ctg 2173
 Ala Asp Val Pro Tyr Val Leu
 435 440

gtg aag acc aat atg gtg gtc acc agc gta gcc atg aag ccg tat gaa 2221
 Val Lys Thr Asn Met Val Val Thr Ser Val Ala Met Lys Pro Tyr Glu
 445 450 455

gtc acc ccg acg cgc atg ctg gtc tgc ggc atc gcc gcc aaa ctg ggc 2269
 Val Thr Pro Thr Arg Met Leu Val Cys Gly Ile Ala Ala Lys Leu Gly
 460 465 470

gcc gcg gcc agc agc ccg gac gcg cac gtg ccg ttc tgc ttc ggc aag 2317
 Ala Ala Ala Ser Ser Pro Asp Ala His Val Pro Phe Cys Phe Gly Lys

475	480	485	
gat ctc aag cgt ccc ggc agc agt ccc atg gaa gtc atg ttg cgc gcc			2365
Asp Leu Lys Arg Pro Gly Ser Ser Pro Met Glu Val Met Leu Arg Ala			
490	495	500	
gtc ttc atg caa caa cgg ccg ctg cgc atg ttt ctg ggt ccc aag caa			2413
Val Phe Met Gln Gln Arg Pro Leu Arg Met Phe Leu Gly Pro Lys Gln			
505	510	515	520
ctc act ttc gaa ggc aag ccc gcg ctc gaa ctg atc cgg atg gtc gaa			2461
Leu Thr Phe Glu Gly Lys Pro Ala Leu Glu Leu Ile Arg Met Val Glu			
525	530	535	
tgc agc ggc aag cag gat tgc ccctgaaggc gaaccccatg cataccatcg			2512
Cys Ser Gly Lys Gln Asp Cys			
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catccatcct gttgtccgtg ctcgccatat acagcccggc tgac gtc gcc gcc ttg			2568
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ccg acc cat ctg tac aag aac ttc act gtc cag gag ctg gcc ttg aaa			2616
Pro Thr His Leu Tyr Lys Asn Phe Thr Val Gln Glu Leu Ala Leu Lys			
550	555	560	
ctg aag ggc aag aat cag gag ttc tgc ctg acc gcc ttc atg tcg ggc			2664
Leu Lys Gly Lys Asn Gln Glu Phe Cys Leu Thr Ala Phe Met Ser Gly			
565	570	575	
aga agc ctg gtc cgg gcg tgc ctg tcc gac gcg gga cac gag cac gac			2712
Arg Ser Leu Val Arg Ala Cys Leu Ser Asp Ala Gly His Glu His Asp			
580	585	590	595
acg tgg ttc gac acc atg ctt ggc ttt gcc ata tcc gcg tat gcg ctc			2760
Thr Trp Phe Asp Thr Met Leu Gly Phe Ala Ile Ser Ala Tyr Ala Leu			
600	605	610	
aag agc cgg atc gcg ctg acg gtg gaa gac tcg ccg tat ccg ggc act			2808
Lys Ser Arg Ile Ala Leu Thr Val Glu Asp Ser Pro Tyr Pro Gly Thr			
615	620	625	
ccc ggc gat ctg ctc gaa ctg cag atc tgc ccg ctc aac gga tat tgc			2856
Pro Gly Asp Leu Leu Glu Leu Gln Ile Cys Pro Leu Asn Gly Tyr Cys			
630	635	640	
gaatgaaccc ttccggaggt ttcgacgttt ccgcgcaatc cgcttgagac gatcttccgc			2916

cctggttcca ttccgggaac accgcaacat gctgatcaac aacaagaagc tgcttcatca 2976

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Ala Val Ala
645

cca ggc atc gtc atc ccg ccg aag gca ctg ttc acc caa cag ggc ggc 3082
Pro Gly Ile Val Ile Pro Pro Lys Ala Leu Phe Thr Gln Gln Gly Gly
650 655 660

gcc tat gga cgc tgc ccg aac gga acc cgc gcc ttg acc gtg gcc gaa 3130
Ala Tyr Gly Arg Cys Pro Asn Gly Thr Arg Ala Leu Thr Val Ala Glu
665 670 675

ctg cgc ggc aac gcc gaa ttg cag acg tat ttg cgc cag ata acg ccc 3178
Leu Arg Gly Asn Ala Glu Leu Gln Thr Tyr Leu Arg Gln Ile Thr Pro
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Tyr Gly Gly Ile Ile Lys Asp Ala Pro Pro Gly Ala Gly Phe Ile Tyr
715 720 725

cgc gaa act ttc tgc atc acg acc ata tac aag acc ggg caa ccg gct 3322
Arg Glu Thr Phe Cys Ile Thr Thr Ile Tyr Lys Thr Gly Gln Pro Ala
730 735 740

gcg gat cac tac tac agc aag gtc acg gcc acg cgc ctg ctc gcc agc 3370
Ala Asp His Tyr Tyr Ser Lys Val Thr Ala Thr Arg Leu Leu Ala Ser
745 750 755

acc aac agc agg ctg tgc gcg gta ttc gtc agg gac ggg caa tcg gtc 3418
Thr Asn Ser Arg Leu Cys Ala Val Phe Val Arg Asp Gly Gln Ser Val
760 765 770

atc gga gcc tgc gcc agc ccg tat gaa ggc agg tac aga gac atg tac 3466
Ile Gly Ala Cys Ala Ser Pro Tyr Glu Gly Arg Tyr Arg Asp Met Tyr
775 780 785 790

gac gcg ctg cgg cgc ctg ctg tac atg atc tat atg tcc ggc ctt gcc 3514
Asp Ala Leu Arg Arg Leu Leu Tyr Met Ile Tyr Met Ser Gly Leu Ala
795 800 805

gta cgc gtc cac gtc agc aag gaa gag cag tat tac gac tac gag gac 3562
Val Arg Val His Val Ser Lys Glu Glu Gln Tyr Tyr Asp Tyr Glu Asp

810	815	820	
gcc aca ttc cag acc tat gcc ctc acc ggc att tcc ctc tgc aac ccg			3610
Ala Thr Phe Gln Thr Tyr Ala Leu Thr Gly Ile Ser Leu Cys Asn Pro			
825	830	835	

gca gcg tcg ata tgctgagccg ccggctcgga tctgttcgcc tgtccatgtt	3662
Ala Ala Ser Ile	
840	

tttccttgac ggataccgcg aatgaatccc ttgaaagact tgagagcatc gctaccgcgc	3722
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<212> PRT

<213> Bordetella pertussis

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35 40 45	
Ala Phe Val Ser Thr Ser Ser Arg Arg Tyr Thr Glu Val Tyr Leu	
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 <213> Bordetella pertussis

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 20 25 30
 Val Ala Glu Leu Arg Gly Asn Ala Glu Leu Gln Thr Tyr Leu Arg Gln
 35 40 45
 Ile Thr Pro Gly Trp Ser Ile Tyr Gly Leu Tyr Asp Gly Thr Tyr Leu
 50 55 60
 Gly Gln Ala Tyr Gly Gly Ile Ile Lys Asp Ala Pro Pro Gly Ala Gly
 65 70 75 80
 Phe Ile Tyr Arg Glu Thr Phe Cys Ile Thr Thr Ile Tyr Lys Thr Gly
 85 90 95
 Gln Pro Ala Ala Asp His Tyr Tyr Ser Lys Val Thr Ala Thr Arg Leu
 100 105 110
 Leu Ala Ser Thr Asn Ser Arg Leu Cys Ala Val Phe Val Arg Asp Gly
 115 120 125
 Gln Ser Val Ile Gly Ala Cys Ala Ser Pro Tyr Glu Gly Arg Tyr Arg
 130 135 140
 Asp Met Tyr Asp Ala Leu Arg Arg Leu Leu Tyr Met Ile Tyr Met Ser
 145 150 155 160
 Gly Leu Ala Val Arg Val His Val Ser Lys Glu Glu Gln Tyr Tyr Asp
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 Tyr Glu Asp Ala Thr Phe Gln Thr Tyr Ala Leu Thr Gly Ile Ser Leu
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 Cys Asn Pro Ala Ala Ser Ile
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 <212> PRT
 <213> Bordetella pertussis

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35	40	45
Pro Glu Asp Val Phe Gln Asn Gly Phe Thr Ala Trp Gly Asn Asn Asp		
50	55	60
Asn Val Leu Asp His Leu Thr Gly Arg Ser Cys Gln Val Gly Ser Ser		
65	70	75 80
Asn Ser Ala Phe Val Ser Thr Ser Ser Ser Arg Arg Tyr Thr Glu Val		
85	90	95
Tyr Leu Glu His Arg Met Gln Glu Ala Val Glu Ala Glu Arg Ala Gly		
100	105	110
Arg Gly Thr Gly His Phe Ile Gly Tyr Ile Tyr Glu Val Arg Ala Asp		
115	120	125
Asn Asn Phe Tyr Gly Ala Ala Ser Ser Tyr Phe Glu Tyr Val Asp Thr		
130	135	140
Tyr Gly Asp Asn Ala Gly Arg Ile Leu Ala Gly Ala Leu Ala Thr Tyr		
145	150	155 160
Gln Ser Glu Tyr Leu Ala His Arg Arg Ile Pro Pro Glu Asn Ile Arg		
165	170	175
Arg Val Thr Arg Val Tyr His His Gly Ile Thr Gly Glu Thr Thr Thr		
180	185	190
Thr Glu Tyr Ser Asn Ala Arg Tyr Val Ser Gln Gln Thr Arg Ala Asn		
195	200	205
Pro Asn Pro Tyr Thr Ser Arg Arg Ser Val Ala Ser Ile Val Gly Thr		
210	215	220
Leu Val Arg Met Ala Pro Val Ile Ser Ala Cys Met Ala Arg Gln Ala		
225	230	235 240
Glu Ser Ser Glu Ala Met Ala Ala Trp Ser Glu Arg Ala Gly Glu Ala		
245	250	255
Met Val Leu Val Tyr Tyr Glu Ser Ile Ala Tyr Ser Phe Val Met Pro		
260	265	270
Ile Asp Arg Lys Thr Leu Cys His Leu Leu Ser Val Leu Pro Leu Ala		

275					280					285						
Leu	Leu	Gly	Ser	His	Val	Ala	Arg	Ala	Ser	Thr	Pro	Gly	Ile	Val	Ile	
290					295					300						
Pro	Pro	Gln	Glu	Gln	Ile	Thr	Gln	His	Gly	Ser	Pro	Tyr	Gly	Arg	Cys	
305					310					315					320	
Ala	Asn	Lys	Thr	Arg	Ala	Leu	Thr	Val	Ala	Glu	Leu	Arg	Gly	Ser	Gly	
325					330					335						
Asp	Leu	Gln	Glu	Tyr	Leu	Arg	His	Val	Thr	Arg	Gly	Trp	Ser	Ile	Phe	
340					345					350						
Ala	Leu	Tyr	Asp	Gly	Thr	Tyr	Leu	Gly	Gly	Glu	Tyr	Gly	Gly	Val	Ile	
355					360					365						
Lys	Asp	Gly	Thr	Pro	Gly	Gly	Ala	Phe	Asp	Leu	Lys	Thr	Thr	Phe	Cys	
370					375					380						
Ile	Met	Thr	Thr	Ala	His	Thr	Gly	Gln	Pro	Ala	Thr	Asp	His	Val	Tyr	
385					390					395					400	
Ser	His	Val	Thr	Ala	Thr	Arg	Leu	Leu	Ser	Ser	Thr	His	Ser	Arg	Leu	
405					410					415						
Cys	Ala	Val	Phe	Val	Arg	Ser	Gly	Gln	Pro	Val	Ile	Gly	Ala	Cys	Thr	
420					425					430						
Ser	Pro	Tyr	Asp	Gly	Lys	Tyr	Trp	Ser	His	Tyr	Ser	Arg	Leu	Arg	Lys	
435					440					445						
Met	Leu	Tyr	Leu	Ile	Tyr	Val	Ala	Gly	Ile	Ser	Val	Arg	Val	His	Val	
450					455					460						
Ser	Lys	Glu	Glu	Gln	Tyr	Tyr	Asp	Tyr	Glu	Asp	Ala	Thr	Phe	Glu	Thr	
465					470					475					480	
Tyr	Ala	Leu	Thr	Gly	Ile	Ser	Ile	Cys	His	Pro	Gly	Ser	Ser	Leu	Cys	
485					490					495						
Val	Ala	Trp	Leu	Leu	Ala	Ser	Gly	Ala	Met	Thr	His	Leu	Ser	Pro	Ala	
500					505					510						
Leu	Ala	Asp	Val	Pro	Tyr	Val	Leu	Val	Lys	Thr	His	His	Val	Val	Thr	
515					520					525						
Ser	Val	Ala	His	Lys	Pro	Val	Glu	Val	Thr	Pro	Thr	Arg	Met	Leu	Val	

530	535	540
Cys Gly Ile Ala Ala Lys Leu Gly Ala Ala Ala Ser Ser Pro Asp Ala		
545	550	555 560
His Val Pro Phe Cys Phe Gly Lys Asp Leu Lys Arg Pro Gly Ser Ser		
565	570	575
Pro His Glu Val Met Leu Arg Ala Val Phe Met Gln Gln Arg Pro Leu		
580	585	590
Arg Met Phe Leu Gly Pro Lys Gln Leu Thr Phe Glu Gly Lys Pro Ala		
595	600	605
Leu Glu Leu Ile Arg Met Val Glu Cys Ser Gly Lys Gln Asp Cys Pro		
610	615	620
Val Phe Met His Thr Ile Ala Ser Ile Leu Leu Ser Val Leu Gly Ile		
625	630	635 640
Tyr Ser Pro Ala Asp Val Ala Gly Leu Pro Thr His Leu Tyr Lys Asn		
645	650	655
Phe Thr Val Gln Glu Leu Ala Leu Lys Leu Lys Gly Lys Asn Gln Glu		
660	665	670
Phe Cys Leu Thr Ala Phe His Ser Gly Arg Ser Leu Val Arg Ala Cys		
675	680	685
Leu Ser Asp Ala Gly His Glu His Asp Thr Trp Phe Asp Thr Met Leu		
690	695	700
Gly Phe Ala Ile Ser Ala Tyr Ala Leu Lys Ser Arg Ile Ala Leu Thr		
705	710	715 720
Val Glu Asp Ser Pro Tyr Pro Gly Thr Pro Gly Asp Leu Leu Glu Leu		
725	730	735
Gln Ile Cys Pro Leu Asn Gly Tyr Cys Glu Val Phe Met Leu Ile Asn		
740	745	750
Asn Lys Lys Leu Leu His His Ile Leu Pro Ile Leu Val Leu Ala Leu		
755	760	765
Leu Gly Met Arg Thr Ala Gln Ala Val Ala Pro Gly Ile Val Ile Pro		
770	775	780
Pro Lys Ala Leu Phe Thr Gln Gln Gly Gly Ala Tyr Gly Arg Cys Pro		

785	790	795	800
Asn Gly Thr Arg Ala Leu Thr Val Ala Glu Leu Arg Gly Asn Ala Glu	805	810	815
Leu Gln Thr Tyr Leu Arg Gln Ile Thr Pro Gly Trp Ser Ile Tyr Gly	820	825	830
Leu Tyr Asp Gly Thr Tyr Leu Gly Gln Ala Tyr Gly Gly Ile Ile Lys	835	840	845
Asp Ala Pro Pro Gly Ala Gly Phe Ile Tyr Arg Glu Thr Phe Cys Ile	850	855	860
Thr Thr Ile Tyr Lys Thr Gly Gln Pro Ala Ala Asp His Tyr Tyr Ser	865	870	875
Lys Val Thr Ala Thr Arg Leu Leu Ala Ser Thr Asn Ser Arg Leu Cys	885	890	895
Ala Val Phe Val Arg Asp Gly Gln Ser Val Ile Gly Ala Cys Ala Ser	900	905	910
Pro Tyr Glu Gly Arg Tyr Arg Asp His Tyr Asp Ala Leu Arg Arg Leu	915	920	925
Leu Tyr Met Ile Tyr Met Ser Gly Leu Ala Val Arg Val His Val Ser	930	935	940
Lys Glu Glu Gln Tyr Tyr Asp Tyr Glu Asp Ala Thr Phe Gln Thr Tyr	945	950	955
Ala Leu Thr Gly Ile Ser Leu Cys Asn Pro Ala Ala Ser Ile Cys Val	965	970	975

<210> 12

<211> 8

<212> PRT

<213> Bordetella pertussis

<400> 12

Tyr Arg Tyr Asp Ser Arg Pro Pro

1

5

<210> 13
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<213> *Vibrio cholerae*

<400> 13
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